REMARKS

Claim Amendments

Claims 1-40 were pending. Claims 1, 7-11, 14 and 38 have been amended and claims 2-6, 12-13 and 15-34 have been canceled. Accordingly, Claims 1, 7-11, 14 and 35-38 remain pending.

No new matter has been added by way of the foregoing amendment, which has been made solely to expedite prosecution and in no way should be viewed as acquiescence to any rejection. Applicants reserve the right to pursue the claims as originally filed in this or subsequent applications.

Restriction Requirement

The Examiner has required restriction between the following inventions in the above-identified application:

Group 1: Claims 1-4, 7-8, drawn to a *mouse MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, classified in class 530, subclass 350;

Group 2: Claims 1-3, 5, 8, 39-40, drawn to a *human MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, or has kinase activity, classified in class 530, subclass 350;

Group 3: Claims 1-3, 6, 8, drawn to *rat MEKK1 protein* or a fragment thereof, which MEKK1 mediates apoptosis, classified in class 530, subclass 350;

Group 4: Claims 9-14, drawn to a *variant mouse MEKK1 protein* or a fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 350;

Group 5: Claims 9-13, 15, drawn to a *variant human MEKK1 protein* or a fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 350;

Group 6: Claims 9-13, 16, a *variant rat MEKK1 protein* or a fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 350;

Group 7: Claims 17-20, 23-24, 31, 33, drawn to a *nucleic acid encoding a mouse MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, classified in class 530, subclass 23.1;

Group 8: Claims 17-19, 21, 23-24, 31, 33, drawn to a *nucleic acid encoding a human MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, classified in class 530, subclass 23.1;

Group 9: Claims 17-19, 22-24, 31, 33, drawn to a *nucleic acid encoding a rat MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, classified in class 530, subclass 23.1;

Group 10: Claims 25-28, 32, 34, drawn to a *nucleic acid encoding a variant mouse MEKK1 protein* or fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 23.1;

Group 11: Claims 25-27, 29, 32, 34, drawn to a *nucleic acid encoding a variant human MEKK1 protein* or fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 23.1;

Group 12: Claims 25-27, 30, 32, 34, drawn to a *nucleic acid encoding a variant rat MEKK1 protein* or fragment thereof, having substitutions, such that the MEKK1 is resistant to proteolysis, classified in class 530, subclass 23.1;

Group 13: Claim 35, drawn to a *method for stimulating apoptosis*, using an expressing vector encoding a *mouse MEKK1 active fragment*, classified in class 514, subclass 44;

Group 14: Claim 35, drawn to a *method for stimulating apoptosis*, using an expressing vector encoding a *human MEKK1 active fragment*, classified in class 514, subclass 44;

Group 15: Claim 35, drawn to a *method for stimulating apoptosis*, using an expressing vector encoding a *rat MEKK1 active fragment*, classified in class 514, subclass 44;

Group 16: Claim 36, drawn to a *method for inhibiting apoptosis*, using a expressing vector encoding a *mouse protease-resistant MEKK1 protein*, classified in class 514, subclass 44;

Group 17: Claim 36, drawn to a *method for inhibiting apoptosis*, using a expressing vector encoding a *human protease-resistant MEKK1 protein*, classified in class 514, subclass 44;

Group 18: Claim 36, drawn to a *method for inhibiting apoptosis*, using a expressing vector encoding a *rat protease-resistant MEKK1 protein*, classified in class 514, subclass 44;

Group 19: Claim 37, drawn to a *method for generating a mouse MEKK1 active fragment*, classified in class 435, subclass 7.1;

Group 20: Claim 37, drawn to a *method for generating a human MEKK1 active fragment*, classified in class 435, subclass 7.1;

Group 21: Claim 37, drawn to a *method for generating a rat MEKK1 active fragment*, classified in class 435, subclass 7.1;

Group 22: Claim 38, drawn to a *method for identifying a compound* that modulates the apoptotic activity of a *mouse active MEKK1 fragment*, classified in class 435, subclass 7.1;

Group 23: Claim 38, drawn to a *method for identifying a compound* that modulates the apoptotic activity of a *human active MEKK1 fragment*, classified in class 435, subclass 7.1; and

Group 24: Claim 38, drawn to a *method for identifying a compound* that modulates the apoptotic activity of a *rat active MEKK1 fragment*, classified in class 435, subclass 7.1.

Accordingly, Applicants hereby elect, with traverse, Group 1 (claims 1-4 and 7-8) drawn to a *mouse MEKK1 protein* or fragment thereof, which MEKK1 mediates apoptosis, for continued examination.

Applicants respectfully traverse the restriction requirement with respect to Groups 1-3 and submit that since these groups are drawn to structurally similar subject matter, they should

be re-grouped as one single Group, *i.e.*, Group 1. Further, to clarify the structural similarity between these Groups, claim 1 has been amended to specify an isolated fragment having 95% identity to an amino acid sequence consisting of about amino acids 875-1493 of SEQ ID NO:3. Similarly, claim 8 has been amended to specify an isolated polypeptide comprising an amino acid sequence set forth in SEQ ID NO:3 or an amino acid sequence 95% identical thereto. As such, the subject matter of Groups 1-3 should properly be re-grouped as one single group.

Moreover, Applicants respectfully traverse the restriction requirement between linked Groups 1-3 and linked Groups 4-6. Applicants submit that Groups 4-6 should properly be included in Group 1 based on the common shared utility (*i.e.*, ability to mediate apoptosis) and the high degree of homology shared by the claimed proteins and corresponding variants. As evidenced by the enclosed sequence alignment (enclosed herewith as Appendix A), the full-length MEKK protein, the MEKK proteins containing mutations at residues 871-874 and the active fragment (comprising amino acids residues 875-1493) are highly homologous and therefore should be re-grouped with elected Group 1.

Applicants further note that, once the product claims are found allowable, the nonelected process claim (*e.g.*, Groups 22-24, *i.e.*, claim 38) will be rejoined in accordance with MPEP 821.04.

The Examiner has further required election of MEKK1.1 or MEKK1.2 as a species in the above-identified application. Accordingly, Applicants hereby elect the species of MEKK1 as set forth as SEQ ID NO:3 (previously referred to as "MEKK1.2") for continued examination. All of the pending claims, as amended to clarify the structural and functional relatedness of the claimed subject matter, read on the elected species. Further, Applicants respectfully submit that Applicants will be entitled to consideration of claims to additional species which are written in dependent form or otherwise include all the limitations of an allowed generic claim as provided by 37 C.F.R. § 1.141 *et seq*.

CONCLUSION

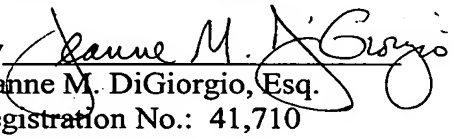
If the Examiner believes that a telephone conversation with Applicants' Attorney would be helpful in expediting prosecution of this application, the Examiner is invited to call the undersigned at (617) 227-7400.

The Director is hereby authorized to charge any deficiency in the fees filed, asserted to be filed or which should have been filed herewith (or with any paper hereafter filed in this application by this firm) to our Deposit Account No. 12-0080, under Order No. CPI-042CN2. A duplicate copy of this paper is enclosed.

In view of the above amendment, applicant believes the pending application is in condition for allowance.

Dated: March 12, 2007

Respectfully submitted,

By 

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Appendix A

CLUSTAL W (1.82) multiple sequence alignment

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MEKK            MAAAAGDRASSSGFPGAAAAASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERAD
871             MAAAAGDRASSSGFPGAAAAASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERAD
871-874         MAAAAGDRASSSGFPGAAAAASPEAGGGGGGGGALQGSGAPAAGAAGLLREPGSAGRERAD
Active          ------------------------------------------------------------

MEKK            WRRRQLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPEPADAAAGASRFQPAAGPPPPG
871             WRRRQLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPEPADAAAGASRFQPAAGPPPPG
871-874         WRRRQLRKVRSVELDQLPEQPLFLAAASPPCPSTSPSPEPADAAAGASRFQPAAGPPPPG
Active          ------------------------------------------------------------

MEKK            AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERMI
871             AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERMI
871-874         AASRCGSHSAELAAARDSGARSPAGAEPPSAAAPSGREMENKETLKGLHKMEDRPEERMI
Active          ------------------------------------------------------------

MEKK            REKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEVNNLAAEPQGEGQAGSAAPAP
871             REKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEVNNLAAEPQGEGQAGSAAPAP
871-874         REKLKATCMPAWKHEWLERRNRRGPVVVKPIPIKGDGSEVNNLAAEPQGEGQAGSAAPAP
Active          ------------------------------------------------------------

MEKK            KGRRSPSPGSSPSGRSVKPESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS
871             KGRRSPSPGSSPSGRSVKPESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS
871-874         KGRRSPSPGSSPSGRSVKPESPGVRRKRVSPVPFQSGRITPPRRAPSPDGFSPYSPEETS
Active          ------------------------------------------------------------

MEKK            RRVNKVMRARLYLLQQIGPNSFLIGGDSPDNKYRVFIGPQNCSCGRGAFCIHLLFVMLRV
871             RRVNKVMRARLYLLQQIGPNSFLIGGDSPDNKYRVFIGPQNCSCGRGAFCIHLLFVMLRV
871-874         RRVNKVMRARLYLLQQIGPNSFLIGGDSPDNKYRVFIGPQNCSCGRGAFCIHLLFVMLRV
Active          ------------------------------------------------------------

MEKK            FQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSS
871             FQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSS
871-874         FQLEPSDPMLWRKTLKNFEVESLFQKYHSRRSSRIKAPSRNTIQKFVSRMSNSHTLSSSS
Active          ------------------------------------------------------------

MEKK            TSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHHCMSIWAEECRRNREP
871             TSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHHCMSIWAEECRRNREP
871-874         TSTSSSENSIKDEEEQMCPICLLGMLDEESLTVCEDGCRNKLHHHCMSIWAEECRRNREP
Active          ------------------------------------------------------------

MEKK            LICPLCRSKWRSHDFYSHELSSPVESPASLRAVQQPSSPQQPVAGSQRRNQESSFNLTHF
871             LICPLCRSKWRSHDFYSHELSSPVESPASLRAVQQPSSPQQPVAGSQRRNQESSFNLTHF
871-874         LICPLCRSKWRSHDFYSHELSSPVESPASLRAVQQPSSPQQPVAGSQRRNQESSFNLTHF
Active          ------------------------------------------------------------

MEKK            GTQQIPSAYKDLAEPWIQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLANGESTG
871             GTQQIPSAYKDLAEPWIQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLANGESTG
871-874         GTQQIPSAYKDLAEPWIQVFGMELVGCLFSRNWNVREMALRRLSHDVSGALLLANGESTG
Active          ------------------------------------------------------------

MEKK            NSGGGSGGSLSAGAASGSSQPSISGDVVEACCSVLSIVCADPVYKVYVAALKTLRAMLVY
871             NSGGGSGGSLSAGAASGSSQPSISGDVVEACCSVLSIVCADPVYKVYVAALKTLRAMLVY
871-874         NSGGGSGGSLSAGAASGSSQPSISGDVVEACCSVLSIVCADPVYKVYVAALKTLRAMLVY
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Active          ------------------------------------------------------------

MEKK            TPCHSLAERIKLQRLLRPVVDTILVKCADANSRTSQLSISTVLELCKGQAGELAVGREIL
871             TPCHSLAERIKLQRLLRPVVDTILVKCADANSRTSQLSISTVLELCKGQAGELAVGREIL
871-874         TPCHSLAERIKLQRLLRPVVDTILVKCADANSRTSQLSISTVLELCKGQAGELAVGREIL
Active          ------------------------------------------------------------

MEKK            KAGSIGVGGVDYVLSCILGNQAESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQA
871             KAGSIGVGGVDYVLSCILGNQAESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQA
871-874         KAGSIGVGGVDYVLSCILGNQAESNNWQELLGRLCLIDRLLLEFPAEFYPHIVSTDVSQA
Active          ------------------------------------------------------------

MEKK            EPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTAVPAVFSKLVTMLNAS
871             EPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTAVPAVFSKLVTMLNAS
871-874         EPVEIRYKKLLSLLTFALQSIDNSHSMVGKLSRRIYLSSARMVTAVPAVFSKLVTMLNAS
Active          ------------------------------------------------------------

MEKK            GSTHFTRMRRRLMAIADEVEIAEVIQLGVEDTVDGHQDSLQAVAPTSCLENSSLEHTVHR
871             GSTHFTRMRRRLMAIADEVEIAEVIQLGVEATVDGHQDSLQAVAPTSCLENSSLEHTVHR
871-874         GSTHFTRMRRRLMAIADEVEIAEVIQLGVEAAAAGHQDSLQAVAPTSCLENSSLEHTVHR
Active          ----------------------------------GHQDSLQAVAPTSCLENSSLEHTVHR
                                                   **************************

MEKK            EKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKPAVQTKGRPHSQCLNSSPLS
871             EKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKPAVQTKGRPHSQCLNSSPLS
871-874         EKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKPAVQTKGRPHSQCLNSSPLS
Active          EKTGKGLSATRLSASSEDISDRLAGVSVGLPSSTTTEQPKPAVQTKGRPHSQCLNSSPLS
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MEKK            HAQLMFPAPSAPCSSAPSVPDISKHRPQAFVPCKIPSASPQTQRKFSLQFQRNCSEHRDS
871             HAQLMFPAPSAPCSSAPSVPDISKHRPQAFVPCKIPSASPQTQRKFSLQFQRNCSEHRDS
871-874         HAQLMFPAPSAPCSSAPSVPDISKHRPQAFVPCKIPSASPQTQRKFSLQFQRNCSEHRDS
Active          HAQLMFPAPSAPCSSAPSVPDISKHRPQAFVPCKIPSASPQTQRKFSLQFQRNCSEHRDS
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MEKK            DQLSPVFTQSRPPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFGGGG
871             DQLSPVFTQSRPPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFGGGG
871-874         DQLSPVFTQSRPPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFGGGG
Active          DQLSPVFTQSRPPPSSNIHRPKPSRPVPGSTSKLGDATKSSMTLDLGSASRCDDSFGGGG
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MEKK            NSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPE
871             NSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPE
871-874         NSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPE
Active          NSGNAVIPSDETVFTPVEDKCRLDVNTELNSSIEDLLEASMPSSDTTVTFKSEVAVLSPE
                ************************************************************

MEKK            KAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQLQVENGEDIIII
871             KAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQLQVENGEDIIII
871-874         KAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQLQVENGEDIIII
Active          KAENDDTYKDDVNHNQKCKEKMEAEEEEALAIAMAMSASQDALPIVPQLQVENGEDIIII
                ************************************************************

MEKK            QQDTPETLPGHTKAKQPYREDAEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRN
871             QQDTPETLPGHTKAKQPYREDAEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRN
871-874         QQDTPETLPGHTKAKQPYREDAEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRN
Active          QQDTPETLPGHTKAKQPYREDAEWLKGQQIGLGAFSSCYQAQDVGTGTLMAVKQVTYVRN
                ************************************************************

MEKK            TSSEQEEVVEALREEIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYG
871             TSSEQEEVVEALREEIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYG
871-874         TSSEQEEVVEALREEIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYG
Active          TSSEQEEVVEALREEIRMMGHLNHPNIIRMLGATCEKSNYNLFIEWMAGGSVAHLLSKYG
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MEKK               AFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKG
871                AFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKG
871-874            AFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKG
Active             AFKESVVINYTEQLLRGLSYLHENQIIHRDVKGANLLIDSTGQRLRIADFGAAARLASKG
                   ************************************************************

MEKK               TGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLA
871                TGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLA
871-874            TGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLA
Active             TGAGEFQGQLLGTIAFMAPEVLRGQQYGRSCDVWSVGCAIIEMACAKPPWNAEKHSNHLA
                   ************************************************************

MEKK               LIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQDRPPSRELLKHPVFRTTW
871                LIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQDRPPSRELLKHPVFRTTW
871-874            LIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQDRPPSRELLKHPVFRTTW
Active             LIFKIASATTAPSIPSHLSPGLRDVAVRCLELQPQDRPPSRELLKHPVFRTTW
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